SEQUENCE LISTING

<110> Duprat, Fabrice
     Lesage, Florian
     Fink, Michel
     Lazdunski, Michel

<120> FAMILY OF MAMMALIAN POTASSIUM CHANNELS, THEIR CLONING
     AND THEIR USE, ESPECIALLY FOR THE SCREENING OF DRUGS

<130> 1201-CIP-DIV-2-00

<141> 2001-08-24

<150> 09/144,914
<151> 1998-09-01

<150> 08/749,816
<151> 1996-11-15

<150> 60/095,234
<151> 1998-08-04

<150> FR 96/01565
<151> 1996-02-08

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<170> PatentIn Ver. 2.0

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cgcgctccgg ccggtctgcg gcgttggcct tggctttggc tttggcggcg gcggtggaga 180

ag atg ctg cag tcc ctg gcc ggc agc tcg tgc gtg cgc ctg gtg gag   227
   Met Leu Gln Ser Leu Ala Gly Ser Ser Cys Val Arg Leu Val Glu
    1   5   10   15

cgg cac cgc tcg gcc tgg tgc ttc ggc ttc ctg gtg ctg ggc tac ttg   275
Arg His Arg Ser Ala Trp Cys Phe Gly Phe Leu Val Leu Gly Tyr Leu
                20   25   30

ctc tac ctg gtc ttc ggc gca gtg gtc ttc tcc tcg gtg gag ctg ccc   323
Leu Tyr Leu Val Phe Gly Ala Val Val Phe Ser Ser Val Glu Leu Pro
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tat gag gac ctg ctg cgc cag gag ctg cgc aag ctg aag cga cgc ttc    371
Tyr Glu Asp Leu Leu Arg Gln Glu Leu Arg Lys Leu Lys Arg Arg Phe
        50                  55                  60

ttg gag gag cac gag tgc ctg tct gag cag cag ctg gag cag ttc ctg    419
Leu Glu Glu His Glu Cys Leu Ser Glu Gln Gln Leu Glu Gln Phe Leu
        65                  70                  75

ggc cgg gtg ctg gag gcc agc aac tac ggc gtg tcg gtg ctc agc aac    467
Gly Arg Val Leu Glu Ala Ser Asn Tyr Gly Val Ser Val Leu Ser Asn
80                  85                  90                  95

gcc tcg ggc aac tgg aac tgg gac ttc acc tcc gcg ctc ttc ttc gcc    515
Ala Ser Gly Asn Trp Asn Trp Asp Phe Thr Ser Ala Leu Phe Phe Ala
                    100                 105                 110

agc acc gtg ctc tcc acc aca ggt tat ggc cac acc gtg ccc ttg tca    563
Ser Thr Val Leu Ser Thr Thr Gly Tyr Gly His Thr Val Pro Leu Ser
                115                 120                 125

gat gga ggt aag gcc ttc tgc atc atc tac tcc gtc att ggc att ccc    611
Asp Gly Gly Lys Ala Phe Cys Ile Ile Tyr Ser Val Ile Gly Ile Pro
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ttc acc ctc ctg ttc ctg acg gct gtg gtc cag cgc atc acc gtg cac    659
Phe Thr Leu Leu Phe Leu Thr Ala Val Val Gln Arg Ile Thr Val His
        145                 150                 155

gtc acc cgc agg ccg gtc ctc tac ttc cac atc cgc tgg ggc ttc tcc    707
Val Thr Arg Arg Pro Val Leu Tyr Phe His Ile Arg Trp Gly Phe Ser
160                 165                 170                 175

aag cag gtg gtg gcc atc gtc cat gcc gtg ctc ctt ggg ttt gtc act    755
Lys Gln Val Val Ala Ile Val His Ala Val Leu Leu Gly Phe Val Thr
                    180                 185                 190

gtg tcc tgc ttc ttc ttc atc ccg gcc gct gtc ttc tca gtc ctg gag    803
Val Ser Cys Phe Phe Phe Ile Pro Ala Ala Val Phe Ser Val Leu Glu
                195                 200                 205

gat gac tgg aac ttc ctg gaa tcc ttt tat ttt tgt ttt att tcc ctg    851
Asp Asp Trp Asn Phe Leu Glu Ser Phe Tyr Phe Cys Phe Ile Ser Leu
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agc acc att ggc ctg ggg gat tat gtg cct ggg gaa ggc tac aat caa    899
Ser Thr Ile Gly Leu Gly Asp Tyr Val Pro Gly Glu Gly Tyr Asn Gln
        225                 230                 235

aaa ttc aga gag ctc tat aag att ggg atc acg tgt tac ctg cta ctt    947
Lys Phe Arg Glu Leu Tyr Lys Ile Gly Ile Thr Cys Tyr Leu Leu Leu
240                 245                 250                 255

ggc ctt att gcc atg ttg gta gtt ctg gaa acc ttc tgt gaa ctc cat    995
Gly Leu Ile Ala Met Leu Val Val Leu Glu Thr Phe Cys Glu Leu His
                260                 265                 270

gag ctg aaa aaa ttc aga aaa atg ttc tat gtg aag aag gac aag gac    1043
Glu Leu Lys Lys Phe Arg Lys Met Phe Tyr Val Lys Lys Asp Lys Asp
            275                 280                 285

gag gat cag gtg cac atc ata gag cat gac caa ctg tcc ttc tcc tcg    1091
Glu Asp Gln Val His Ile Ile Glu His Asp Gln Leu Ser Phe Ser Ser
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Glu Asp Gln Val His Ile Ile Glu His Asp Gln Leu Ser Phe Ser Ser
        290                 295                 300

atc aca gac cag gca gct ggc atg aaa gag gac cag aag caa aat gag   1139
Ile Thr Asp Gln Ala Ala Gly Met Lys Glu Asp Gln Lys Gln Asn Glu
        305                 310                 315

cct ttt gtg gcc acc cag tca tct gcc tgc gtg gat ggc cct gca aac   1187
Pro Phe Val Ala Thr Gln Ser Ser Ala Cys Val Asp Gly Pro Ala Asn
320                 325                 330                 335

cat tgagcgtagg atttgttgca ttatgctaga gcaccagggt cagggtgcaa       1240
His

ggaagaggct taagtatgtt catttttatc agaatgcaaa agcgaaaatt atgtcacttt 1300

aagaaatagc tactgtttgc aatgtcttat taaaaaacaa caaaaaaaga cacatggaac 1360

aaagaagctg tgaccccagc aggatgtcta atatgtgagg aaatgagatg tccacctaaa 1420

attcatatgt gacaaaatta tctcgacctt acataggagg agaatacttg aagcagtatg 1480

ctgctgtggt tagaagcaga ttttatactt ttaactggaa actttggggt ttgcatttag 1540

atcatttagc tgatggctaa atagcaaaat ttatatttag aagcaaaaaa aaaaagcata 1600

gagatgtgtt ttataaatag gtttatgtgt actggtttgc atgtacccac ccaaaatgat 1660

tattttggga gaatctaagt caaactcact atttataatg cataggtaac cattaactat 1720

gtacatataa agtataaata tgtttatatt ctgtacatat ggtttaggtc accagatcct 1780

agtgtagttc tgaaactaag actatagata ttttgtttct tttgatttct ctttatacta 1840

aagaatccag agttgctaca ataaaataag gggaataata aaaaaaaaaa aaaa        1894

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His Arg Ser Ala Trp Cys Phe Gly Phe Leu Val Leu Gly Tyr Leu Leu
                20                  25                  30

Tyr Leu Val Phe Gly Ala Val Val Phe Ser Ser Val Glu Leu Pro Tyr
            35                  40                  45

Glu Asp Leu Leu Arg Gln Glu Leu Arg Lys Leu Lys Arg Arg Phe Leu
        50                  55                  60

Glu Glu His Glu Cys Leu Ser Glu Gln Gln Leu Glu Gln Phe Leu Gly
 65                  70                  75                  80
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Arg Val Leu Glu Ala Ser Asn Tyr Gly Val Ser Val Leu Ser Asn Ala
                85                  90              95

Ser Gly Asn Trp Asn Trp Asp Phe Thr Ser Ala Leu Phe Phe Ala Ser
            100             105             110

Thr Val Leu Ser Thr Thr Gly Tyr Gly His Thr Val Pro Leu Ser Asp
        115             120             125

Gly Gly Lys Ala Phe Cys Ile Ile Tyr Ser Val Ile Gly Ile Pro Phe
    130             135             140

Thr Leu Leu Phe Leu Thr Ala Val Val Gln Arg Ile Thr Val His Val
145             150             155             160

Thr Arg Arg Pro Val Leu Tyr Phe His Ile Arg Trp Gly Phe Ser Lys
            165             170             175

Gln Val Val Ala Ile Val His Ala Val Leu Leu Gly Phe Val Thr Val
            180             185             190

Ser Cys Phe Phe Phe Ile Pro Ala Ala Val Phe Ser Val Leu Glu Asp
        195             200             205

Asp Trp Asn Phe Leu Glu Ser Phe Tyr Phe Cys Phe Ile Ser Leu Ser
    210             215             220

Thr Ile Gly Leu Gly Asp Tyr Val Pro Gly Glu Gly Tyr Asn Gln Lys
225             230             235             240

Phe Arg Glu Leu Tyr Lys Ile Gly Ile Thr Cys Tyr Leu Leu Leu Gly
            245             250             255

Leu Ile Ala Met Leu Val Val Leu Glu Thr Phe Cys Glu Leu His Glu
            260             265             270

Leu Lys Lys Phe Arg Lys Met Phe Tyr Val Lys Lys Asp Lys Asp Glu
        275             280             285

Asp Gln Val His Ile Ile Glu His Asp Gln Leu Ser Phe Ser Ser Ile
    290             295             300

Thr Asp Gln Ala Ala Gly Met Lys Glu Asp Gln Lys Gln Asn Glu Pro
305             310             315             320

Phe Val Ala Thr Gln Ser Ser Ala Cys Val Asp Gly Pro Ala Asn His
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ggacg atg aag cgg cag aac gtg cgc acg ctg gcg ctc atc gtg tgc acc 170
      Met Lys Arg Gln Asn Val Arg Thr Leu Ala Leu Ile Val Cys Thr
      1               5                   10                  15

ttc acc tac ctg ctg gtg ggc gcc gcg gtc ttc gac gcg ctg gag tcg 218
Phe Thr Tyr Leu Leu Val Gly Ala Ala Val Phe Asp Ala Leu Glu Ser
              20                  25                  30

gag ccc gag ctg atc gag cgg cag cgg ctg gag ctg cgg cag cag gag 266
Glu Pro Glu Leu Ile Glu Arg Gln Arg Leu Glu Leu Arg Gln Gln Glu
          35                  40                  45

ctg cgg gcg cgc tac aac ctc agc cag ggc ggc tac gag gag ctg gag 314
Leu Arg Ala Arg Tyr Asn Leu Ser Gln Gly Gly Tyr Glu Glu Leu Glu
      50                  55                  60

cgc gtc gtg ctg cgc ctc aag ccg cac aag gcc ggc gtg cag tgg cgc 362
Arg Val Val Leu Arg Leu Lys Pro His Lys Ala Gly Val Gln Trp Arg
      65                  70                  75

ttc gcc ggc tcc ttc tac ttc gcc atc acc gtc atc acc acc atc ggc 410
Phe Ala Gly Ser Phe Tyr Phe Ala Ile Thr Val Ile Thr Thr Ile Gly
80                  85                  90                  95

tac ggg cac gcg gca ccc agc acg gat ggc ggc aag gtg ttc tgc atg 458
Tyr Gly His Ala Ala Pro Ser Thr Asp Gly Gly Lys Val Phe Cys Met
              100                 105                 110

ttc tac gcg ctg ctg ggc atc ccg ctc acg ctc gtc atg ttc cag agc 506
Phe Tyr Ala Leu Leu Gly Ile Pro Leu Thr Leu Val Met Phe Gln Ser
              115                 120                 125

ctg ggc gag cgc atc aac acc ttg gtg agg tac ctg ctg cac cgc gcc 554
Leu Gly Glu Arg Ile Asn Thr Leu Val Arg Tyr Leu Leu His Arg Ala
          130                 135                 140

aag aag ggg ctg ggc atg cgg cgc gcc gac gtg tcc atg gcc aac atg 602
Lys Lys Gly Leu Gly Met Arg Arg Ala Asp Val Ser Met Ala Asn Met
      145                 150                 155

gtg ctc atc ggc ttc ttc tcg tgc atc agc acg ctg tgc atc ggc gcc 650
Val Leu Ile Gly Phe Phe Ser Cys Ile Ser Thr Leu Cys Ile Gly Ala
160                 165                 170                 175

gcc gcc ttc tcc cac tac gag cac tgg acc ttc ttc cag gcc tac tac 698
Ala Ala Phe Ser His Tyr Glu His Trp Thr Phe Phe Gln Ala Tyr Tyr
              180                 185                 190

tac tgc ttc atc acc ctc acc acc atc ggc ttc ggc gac tac gtg gcg 746
Tyr Cys Phe Ile Thr Leu Thr Thr Ile Gly Phe Gly Asp Tyr Val Ala
              195                 200                 205

ctg cag aag gac cag gcc ctg cag acg cag ccg cag tac gtg gcc ttc 794
Leu Gln Lys Asp Gln Ala Leu Gln Thr Gln Pro Gln Tyr Val Ala Phe
      210                 215                 220
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agc ttc gtc tac atc ctt acg ggc ctc acg gtc atc ggc gcc ttc ctc   842
Ser Phe Val Tyr Ile Leu Thr Gly Leu Thr Val Ile Gly Ala Phe Leu
    225                 230                 235

aac ctc gtg gtg ctg cgc ttc atg acc atg aac gcc gag gac gag aag   890
Asn Leu Val Val Leu Arg Phe Met Thr Met Asn Ala Glu Asp Glu Lys
240                 245                 250                 255

cgc gac gcc gag cac cgc gcg ctg ctc acg cgc aac ggg cag gcg ggc   938
Arg Asp Ala Glu His Arg Ala Leu Leu Thr Arg Asn Gly Gln Ala Gly
                260                 265                 270

ggc ggc gga ggg ggt ggc agc gcg cac act acg gac acc gcc tca tcc   986
Gly Gly Gly Gly Gly Gly Ser Ala His Thr Thr Asp Thr Ala Ser Ser
                275                 280                 285

acg gcg gca gcg ggc ggc ggc ggc ttc cgc aac gtc tac gcg gag gtg  1034
Thr Ala Ala Ala Gly Gly Gly Gly Phe Arg Asn Val Tyr Ala Glu Val
                290                 295                 300

ctg cac ttc cag tcc atg tgc tcg tgc ctg tgg tac aag agc cgc gag  1082
Leu His Phe Gln Ser Met Cys Ser Cys Leu Trp Tyr Lys Ser Arg Glu
    305                 310                 315

aag ctg cag tac tcc atc ccc atg atc atc ccg cgg gac ctc tcc acg  1130
Lys Leu Gln Tyr Ser Ile Pro Met Ile Ile Pro Arg Asp Leu Ser Thr
320                 325                 330                 335

tcc gac acg tgc gtg gag cag agc cac tcg tcg ccg gga ggg ggc ggc  1178
Ser Asp Thr Cys Val Glu Gln Ser His Ser Ser Pro Gly Gly Gly Gly
                340                 345                 350

cgc tac agc gac acg ccc tcg cga cgc tgc ctg tgc agc ggg gcg cca  1226
Arg Tyr Ser Asp Thr Pro Ser Arg Arg Cys Leu Cys Ser Gly Ala Pro
                355                 360                 365

cgc tcc gcc atc agc tcg gtg tcc acg ggt ctg cac agc ctg tcc acc  1274
Arg Ser Ala Ile Ser Ser Val Ser Thr Gly Leu His Ser Leu Ser Thr
    370                 375                 380

ttc cgc ggc ctc atg aag cgc agg agc tcc gtg tgactgcccc gagggacctg 1327
Phe Arg Gly Leu Met Lys Arg Arg Ser Ser Val
    385                 390

gagcacctgg gggcgcgggc gggggacccc tgctgggagg ccaggagact gcccctgctg 1387

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ctatgtccaa gtcacccta ctcagcccca ctccccttcc tcatccccag ctgtgtctcc 1807

caacctccct tcgtgttgtt ttgcatggct ttgcagttat ggagaaagtg gaaacccagc 1867
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gaggttcaag ctaactggcc tccagccaca ttctcatagc aggtaggact tcagccttcc 2047

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gaggattgtt tgagcctggg aggtcgaggc tgtagtgagc cctgattgca ccactgtact 2467

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<223> TASK

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Met Lys Arg Gln Asn Val Arg Thr Leu Ala Leu Ile Val Cys Thr Phe
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Thr Tyr Leu Leu Val Gly Ala Ala Val Phe Asp Ala Leu Glu Ser Glu
                20   25   30

Pro Glu Leu Ile Glu Arg Gln Arg Leu Glu Leu Arg Gln Gln Glu Leu
            35   40   45

Arg Ala Arg Tyr Asn Leu Ser Gln Gly Gly Tyr Glu Glu Leu Glu Arg
        50   55   60

Val Val Leu Arg Leu Lys Pro His Lys Ala Gly Val Gln Trp Arg Phe
65   70   75   80

Ala Gly Ser Phe Tyr Phe Ala Ile Thr Val Ile Thr Thr Ile Gly Tyr
                85   90   95

Gly His Ala Ala Pro Ser Thr Asp Gly Gly Lys Val Phe Cys Met Phe
                100   105   110

Tyr Ala Leu Leu Gly Ile Pro Leu Thr Leu Val Met Phe Gln Ser Leu
            115   120   125

Gly Glu Arg Ile Asn Thr Leu Val Arg Tyr Leu Leu His Arg Ala Lys
        130   135   140

Lys Gly Leu Gly Met Arg Arg Ala Asp Val Ser Met Ala Asn Met Val

Leu Ile Gly Phe Phe Ser Cys Ile Ser Thr Leu Cys Ile Gly Ala Ala
                    165   170   175

Ala Phe Ser His Tyr Glu His Trp Thr Phe Phe Gln Ala Tyr Tyr Tyr
                180   185   190

Cys Phe Ile Thr Leu Thr Thr Ile Gly Phe Gly Asp Tyr Val Ala Leu
                195   200   205

Gln Lys Asp Gln Ala Leu Gln Thr Gln Pro Gln Tyr Val Ala Phe Ser
    210   215   220

Phe Val Tyr Ile Leu Thr Gly Leu Thr Val Ile Gly Ala Phe Leu Asn
225   230   235   240

Leu Val Val Leu Arg Phe Met Thr Met Asn Ala Glu Asp Glu Lys Arg
                245   250   255

Asp Ala Glu His Arg Ala Leu Leu Thr Arg Asn Gly Gln Ala Gly Gly
                260   265   270

Gly Gly Gly Gly Gly Ser Ala His Thr Thr Asp Thr Ala Ser Ser Thr
                275   280   285

Ala Ala Ala Gly Gly Gly Gly Phe Arg Asn Val Tyr Ala Glu Val Leu
    290   295   300

His Phe Gln Ser Met Cys Ser Cys Leu Trp Tyr Lys Ser Arg Glu Lys
305   310   315   320

Leu Gln Tyr Ser Ile Pro Met Ile Ile Pro Arg Asp Leu Ser Thr Ser
                325   330   335

Asp Thr Cys Val Glu Gln Ser His Ser Ser Pro Gly Gly Gly Gly Arg
                340   345   350

Tyr Ser Asp Thr Pro Ser Arg Arg Cys Leu Cys Ser Gly Ala Pro Arg
                355   360   365

Ser Ala Ile Ser Ser Val Ser Thr Gly Leu His Ser Leu Ser Thr Phe
    370   375   380

Arg Gly Leu Met Lys Arg Arg Ser Ser Val
385   390

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<212> PRT
<213> Murine

<220>
<223> TASK

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Leu Val Gly Ala Ala Val Phe Asp Ala Leu Glu Ser Glu Pro Glu Met

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Ile Glu Arg Gln Arg Leu Glu Leu Arg Gln Leu Glu Leu Arg Ala Arg
        35                  40                  45

Tyr Asn Leu Ser Glu Gly Gly Tyr Glu Glu Leu Glu Arg Val Val Leu
        50                  55                  60

Arg Leu Lys Pro His Lys Ala Gly Val Gln Trp Arg Phe Ala Gly Ser
65                  70                  75                  80

Phe Tyr Phe Ala Ile Thr Val Ile Thr Thr Ile Gly Tyr Gly His Ala
                85                  90                  95

Ala Pro Ser Thr Asp Gly Gly Lys Val Phe Cys Met Phe Tyr Ala Leu
            100                 105                 110

Leu Gly Ile Pro Leu Thr Leu Ile Met Phe Gln Ser Leu Gly Glu Arg
            115                 120                 125

Ile Asn Thr Phe Val Arg Tyr Leu Leu His Arg Ala Lys Arg Gly Leu
    130                 135                 140

Gly Met Arg His Ala Glu Val Ser Met Ala Asn Met Val Leu Ile Gly
145                 150                 155                 160

Phe Val Ser Cys Ile Ser Thr Leu Cys Ile Gly Ala Ala Ala Phe Ser
                165                 170                 175

Tyr Tyr Glu Arg Trp Thr Phe Phe Gln Ala Tyr Tyr Tyr Cys Phe Ile
            180                 185                 190

Thr Leu Thr Thr Ile Gly Phe Gly Asp Tyr Val Ala Leu Gln Lys Asp
        195                 200                 205

Gln Ala Leu Gln Thr Gln Pro Gln Tyr Val Ala Phe Ser Phe Val Tyr
    210                 215                 220

Ile Leu Thr Gly Leu Thr Val Ile Gly Ala Phe Leu Asn Leu Val Val
225                 230                 235                 240

Leu Arg Phe Met Thr Met Asn Ala Glu Asp Glu Lys Arg Asp Ala Glu
            245                 250                 255

His Arg Ala Leu Leu Thr His Asn Gly Gln Ala Val Gly Leu Gly Gly
            260                 265                 270

Leu Ser Cys Leu Ser Gly Ser Leu Gly Asp Val Arg Pro Arg Asp Pro
        275                 280                 285

Val Thr Cys Ala Ala Ala Gly Gly Val Gly Val Gly Val Gly Gly
    290                 295                 300

Ser Gly Phe Arg Asn Val Tyr Ala Glu Val Leu His Phe Gln Ser Met
305                 310                 315                 320

Cys Ser Cys Leu Trp Tyr Lys Ser Arg Glu Lys Leu Gln Tyr Ser Ile
            325                 330                 335

Pro Met Ile Ile Pro Arg Asp Leu Ser Thr Ser Asp Thr Cys Val Glu
            340                 345                 350
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His Ser His Ser Ser Pro Gly Gly Gly Gly Arg Tyr Ser Asp Thr Pro
     355   360   365

Ser His Pro Cys Leu Cys Ser Gly Thr Gln Arg Ser Ala Ile Ser Ser
     370   375   380

Val Ser Thr Gly Leu His Ser Leu Ala Ala Phe Arg Gly Leu Met Lys
385   390   395   400

Arg Arg Ser Ser Val
           405

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Ser Thr Met Gln Lys Met Ser Pro Asn Thr Arg Gln Asn Phe Arg Gln
        20   25   30

Asn Val Asn Val Val Val Cys Leu Ser Ala Ala Ile Thr Leu Leu Val
        35   40   45

Phe Asn Leu Ile Gly Ala Gly Ile Phe Tyr Leu Ala Glu Thr Gln Asn
      50   55   60

Ser Ser Glu Ser Leu Asn Glu Asn Ser Glu Val Ser Lys Cys Leu His
  65   70   75   80

Asn Leu Pro Ile Gly Gly Lys Ile Thr Ala Glu Met Lys Ser Lys Leu
        85   90   95

Gly Lys Cys Leu Thr Lys Ser Ser Arg Ile Asp Gly Phe Gly Lys Ala
        100   105   110

Ile Phe Phe Ser Trp Thr Leu Tyr Ser Thr Val Gly Tyr Gly Ser Leu
        115   120   125

Tyr Pro His Ser Thr Leu Gly Arg Tyr Leu Thr Ile Phe Tyr Ser Leu
        130   135   140

Leu Met Ile Pro Val Phe Ile Ala Phe Lys Phe Glu Phe Gly Thr Phe
145   150   155   160

Leu Ala His Phe Leu Val Val Val Ser Asn Arg Thr Arg Leu Ala Val
        165   170   175

Lys Lys Ala Tyr Tyr Lys Leu Ser Gln Asn Pro Glu Asn Ala Glu Thr
        180   185   190

Pro Ser Asn Ser Leu Gln His Asp Tyr Leu Ile Phe Leu Ser Ser Leu
        195   200   205

Leu Leu Cys Ser Ile Ser Leu Leu Ser Ser Ser Ala Leu Phe Ser Ser
    210   215   220

Ile Glu Asn Ile Ser Tyr Leu Ser Ser Val Tyr Phe Gly Ile Ile Thr
225   230   235   240

Met Phe Leu Ile Gly Ile Gly Asp Ile Val Pro Thr Asn Leu Val Trp
            245   250   255

Phe Ser Gly Tyr Cys Met Leu Phe Leu Ile Ser Asp Val Leu Ser Asn
            260   265   270

Gln Ile Phe Tyr Phe Cys Gln Ala Arg Val Arg Tyr Phe Phe His Ile
        275   280   285

Leu Ala Arg Lys Ile Leu Leu Leu Arg Glu Glu Asp Asp Gly Phe Gln
    290   295   300

Leu Glu Thr Thr Val Ser Leu Gln His Ile Pro Ile Ile Asn Ser Gln
305   310   315   320

Cys Met Pro Ser Leu Val Leu Asp Cys Glu Lys Glu Glu Leu Asp Asn
            325   330   335

Asp Glu Lys Leu Ile Ser Ser Leu Thr Ser Thr
            340   345

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<212> PRT
<213> Unknown

<220>
<223> Description of Unknown Organism: TWIK-1 homolog

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Met Thr Val Ser Met Glu Glu Asn Ser Lys Ile Gln Met Leu Ser Ala
  1   5   10   15

Thr Ser Lys Asp Lys Lys Val Ala Thr Asp Arg Ser Leu Leu Asn Lys
            20   25   30

Tyr His Leu Gly Pro Leu Ala Leu His Thr Gly Leu Val Leu Ser Cys
        35   40   45

Val Thr Tyr Ala Leu Gly Gly Ala Tyr Leu Phe Leu Ser Ile Glu His
    50   55   60

Pro Glu Glu Leu Lys Arg Arg Glu Lys Ala Ile Arg Glu Phe Gln Asp
65   70   75   80

Leu Lys Gln Gln Phe Met Gly Asn Ile Thr Ser Gly Ile Glu Asn Ser
            85   90   95

Glu Gln Ser Ile Glu Ile Tyr Thr Lys Lys Leu Ile Leu Met Leu Glu
            100   105   110

Asp Ala His Asn Ala His Ala Phe Glu Tyr Phe Phe Leu Asn His Glu
        115   120   125

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Ile Pro Lys Asp Met Trp Thr Phe Ser Ser Ala Leu Val Phe Thr Thr
    130             135             140

Thr Thr Val Ile Pro Val Gly Tyr Gly Tyr Ile Phe Pro Val Ser Ala
145             150             155             160

Tyr Gly Arg Met Cys Leu Ile Ala Tyr Ala Leu Leu Gly Ile Pro Leu
            165             170             175

Thr Leu Val Thr Met Ala Asp Thr Gly Lys Phe Ala Ala Gln Leu Val
            180             185             190

Thr Arg Trp Phe Gly Asp Asn Asn Met Ala Ile Pro Ala Ala Ile Phe
        195             200             205

Val Cys Leu Leu Phe Ala Tyr Pro Leu Val Val Gly Phe Ile Leu Cys
    210             215             220

Ser Thr Ser Asn Ile Thr Tyr Leu Asp Ser Val Tyr Phe Ser Leu Thr
225             230             235             240

Ser Ile Phe Thr Ile Gly Phe Gly Asp Leu Thr Pro Asp Met Asn Val
            245             250             255

Ile His Met Val Leu Phe Leu Ala Val Gly Val Ile Leu Val Thr Ile
            260             265             270

Thr Leu Asp Ile Val Ala Ala Glu Met Ile Asp Arg Val His Tyr Met
        275             280             285

Gly Arg His Val Gly Lys Ala Lys Glu Leu Ala Gly Lys Met Phe Gln
    290             295             300

Leu Ala Gln Ser Leu Asn Met Lys Gln Gly Leu Val Ser Gly Val Gly
305             310             315             320

Gln Leu His Ala Leu Ala Arg Phe Gly Met Leu Val Gly Arg Glu Glu
            325             330             335

Val Asp Lys Thr Gln Glu Asp Gly Ile Ile Ala Phe Ser Pro Asp Val
            340             345             350

Met Asp Gly Leu Glu Phe Met Asp Thr Leu Ser Ile Tyr Ser Arg Arg
        355             360             365

Ser Arg Arg Ser Ala Glu Asn Ser Ala Arg Asn Leu Phe Leu Ser
    370             375             380


<210> 8
<211> 370
<212> PRT
<213> Murine

<220>
<223> TREK-1

<400> 8
Met Ala Ala Pro Asp Leu Leu Asp Pro Lys Ser Ala Ala Gln Asn Ser
  1             5               10              15
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Lys Pro Arg Leu Ser Phe Ser Ser Lys Pro Thr Val Leu Ala Ser Arg
            20              25              30

Val Glu Ser Asp Ser Ala Ile Asn Val Met Lys Trp Lys Thr Val Ser
            35              40              45

Thr Ile Phe Leu Val Val Val Leu Tyr Leu Ile Ile Gly Ala Ala Val
        50              55              60

Phe Lys Ala Leu Glu Gln Pro Gln Glu Ile Ser Gln Arg Thr Thr Ile
65              70              75              80

Val Ile Gln Lys Gln Thr Phe Ile Ala Gln His Ala Cys Val Asn Ser
                85              90              95

Thr Glu Leu Asp Glu Leu Ile Gln Gln Ile Val Ala Ala Ile Asn Ala
            100             105             110

Gly Ile Ile Pro Leu Gly Asn Ser Ser Asn Gln Val Ser His Trp Asp
            115             120             125

Leu Gly Ser Ser Phe Phe Phe Ala Gly Thr Val Ile Thr Thr Ile Gly
    130             135             140

Phe Gly Asn Ile Ser Pro Arg Thr Glu Gly Gly Lys Ile Phe Cys Ile
145             150             155             160

Ile Tyr Ala Leu Leu Gly Ile Pro Leu Glu Gly Phe Leu Leu Ala Gly
            165             170             175

Val Gly Asp Gln Leu Gly Thr Ile Phe Gly Lys Gly Ile Ala Lys Val
            180             185             190

Glu Asp Thr Phe Ile Lys Trp Asn Val Ser Gln Thr Lys Ile Arg Ile
        195             200             205

Ile Ser Thr Ile Ile Phe Ile Leu Phe Gly Cys Val Leu Phe Val Ala
    210             215             220

Leu Pro Ala Val Ile Phe Lys His Ile Glu Gly Trp Ser Ala Leu Asp
225             230             235             240

Ala Ile Tyr Phe Val Val Ile Thr Leu Thr Thr Ile Gly Phe Gly Asp
            245             250             255

Tyr Val Ala Gly Gly Ser Asp Ile Glu Tyr Leu Asp Phe Tyr Lys Pro
            260             265             270

Val Val Trp Phe Trp Ile Leu Val Gly Leu Ala Tyr Phe Ala Ala Val
        275             280             285

Leu Ser Met Ile Gly Asp Trp Leu Arg Val Ile Ser Lys Lys Thr Lys
    290             295             300

Glu Glu Val Gly Glu Phe Arg Ala His Ala Ala Glu Trp Thr Ala Asn
305             310             315             320

Val Thr Ala Glu Phe Lys Glu Thr Arg Arg Arg Leu Ser Val Glu Ile
            325             330             335
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Tyr Asp Lys Phe Gln Arg Ala Thr Ser Val Lys Arg Lys Leu Ser Ala
            340   345   350

Glu Leu Ala Gly Asn His Asn Gln Glu Leu Thr Pro Cys Met Arg Thr
            355   360   365

Cys Leu
    370

<210> 9
<211> 27
<212> PRT
<213> Homo sapiens

<220>
<223> TWIK-1 P1

<400> 9
Phe Thr Ser Ala Leu Phe Phe Ala Ser Thr Val Leu Ser Thr Thr Gly
    1   5   10   15

Tyr Gly His Thr Val Pro Leu Ser Asp Gly Gly
            20   25

<210> 10
<211> 27
<212> PRT
<213> Homo sapiens

<220>
<223> TWIK-1 P2

<400> 10
Phe Leu Glu Ser Phe Tyr Phe Cys Phe Ile Ser Leu Ser Thr Ile Gly
    1   5   10   15

Leu Gly Asp Tyr Val Pro Gly Glu Gly Tyr Asn
            20   25

<210> 11
<211> 27
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown Organism: P domain of
      representative K+ channel sequence

<220>
<223> TOK-1 P2

<400> 11
Tyr Phe Asn Cys Ile Tyr Phe Cys Phe Leu Cys Leu Leu Thr Ile Gly
    1   5   10   15

Tyr Gly Asp Tyr Ala Pro Arg Thr Gly Ala Gly
            20   25

<210> 12
<211> 27
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown Organism: P domain of
      representative K+ channel sequence

<220>
<223> TOK-1 P1

<400> 12
Tyr Gly Asn Ala Leu Tyr Phe Cys Thr Val Ser Leu Leu Thr Val Gly
 1   5   10   15

Leu Gly Asp Ile Leu Pro Lys Ser Val Gly Ala
            20   25

<210> 13
<211> 27
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown Organism: P domain of
      representative K+ channel sequence

<220>
<223> Slo

<400> 13
Tyr Trp Thr Cys Val Tyr Phe Leu Ile Val Thr Met Ser Thr Val Gly
 1   5   10   15

Tyr Gly Asp Val Tyr Cys Glu Thr Val Leu Gly
            20   25

<210> 14
<211> 27
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown Organism: P domain of
      representative K+ channel sequence

<220>
<223> Shaker

<400> 14
Ile Pro Asp Ala Phe Trp Trp Ala Val Val Thr Met Thr Thr Val Gly
 1   5   10   15

Tyr Gly Asp Met Thr Pro Val Gly Phe Trp Gly
            20   25

<210> 15
<211> 27
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown Organism: P domain of
      representative K+ channel sequence

<220>
<223> Shab

<400> 15
Ile Pro Glu Ala Phe Trp Trp Ala Gly Ile Thr Met Thr Thr Val Gly
 1   5   10   15

Tyr Gly Asp Ile Cys Pro Thr Thr Ala Leu Gly
            20   25

<210> 16
<211> 27
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown Organism: P domain of
      representative K+ channel sequence

<220>
<223> Shal

<400> 16
Ile Pro Ala Ala Phe Trp Tyr Thr Ile Val Thr Met Thr Thr Leu Gly
 1   5   10   15

Tyr Gly Asp Met Val Pro Glu Thr Ile Ala Gly
            20   25

<210> 17
<211> 27
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown Organism: P domain of
      representative K+ channel sequence

<220>
<223> Shaw

<400> 17
Ile Pro Leu Gly Leu Trp Trp Ala Leu Val Thr Met Thr Thr Val Gly
 1   5   10   15

Tyr Gly Asp Met Ala Pro Lys Thr Tyr Ile Gly
            20   25

<210> 18

<211> 27
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown Organism: P domain of
     representative K+ channel sequence

<220>
<223> KAT1

<400> 18
Tyr Val Thr Ala Leu Tyr Trp Ser Ile Thr Thr Leu Thr Thr Thr Gly
 1   5   10   15

Tyr Gly Asp Phe His Ala Glu Asn Pro Arg Glu
            20   25

<210> 19
<211> 27
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown Organism: P domain of
     representative K+ channel sequence

<220>
<223> AKT1

<400> 19
Tyr Val Thr Ser Met Tyr Trp Ser Ile Thr Thr Leu Thr Thr Val Gly
 1   5   10   15

Tyr Gly Asp Ile His Pro Val Asn Thr Lys Glu
            20   25

<210> 20
<211> 27
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown Organism: P domain of
     representative K+ channel sequence

<220>
<223> eag

<400> 20
Tyr Val Thr Ala Leu Tyr Phe Thr Met Thr Cys Met Thr Ser Val Gly
 1   5   10   15

Phe Gly Asn Val Ala Ala Glu Thr Asp Asn Glu
            20   25

<210> 21
<211> 27

<212> PRT
<213> Unknown

<220>
<223> Description of Unknown Organism: P domain of
      representative K+ channel sequence

<220>
<223> ROMK1

<400> 21
Met Thr Ser Ala Phe Leu Phe Ser Leu Glu Thr Gln Val Thr Ile Gly
 1   5   10   15

Tyr Gly Phe Arg Phe Val Thr Glu Gln Cys Ala
            20   25

<210> 22
<211> 27
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown Organism: P domain of
      representative K+ channel sequence

<220>
<223> IRK1

<400> 22
Phe Thr Ala Ala Phe Leu Phe Ser Ile Glu Thr Gln Thr Thr Ile Gly
 1   5   10   15

Tyr Gly Phe Arg Cys Val Thr Asp Glu Cys Pro
            20   25

<210> 23
<211> 27
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown Organism: P domain of
      representative K+ channel sequence

<220>
<223> GIRK1

<400> 23
Phe Pro Ser Ala Phe Leu Phe Phe Ile Glu Thr Glu Ala Thr Ile Gly
 1   5   10   15

Tyr Gly Tyr Arg Tyr Ile Thr Asp Lys Cys Pro
            20   25

<210> 24
<211> 48
<212> DNA

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: antisense
     oligonucleotide complementary to the partial
     mouse cDNA sequence of TASK

<400> 24
caccagcagg taggtgaagg tgcacacgat gagagccaac gtgcgcac   48